

0507 #2

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/053,406

DATE: 02/06/2002

TIME: 09:33:41

Input Set : N:\Crf3\RULE60\10053406.raw

Output Set: N:\CRF3\02062002\J053406.raw

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1 <110> APPLICANT: Debinski, Waldemar
2 Thompson, Jeffrey
3 <120> TITLE OF INVENTION: IL13 MUTANTS
4 <130> FILE REFERENCE: 6460-28
5 <140> CURRENT APPLICATION NUMBER: 10/053,406
6 <141> CURRENT FILING DATE: 2002-01-17
8 <150> PRIOR APPLICATION NUMBER: US/09/679,710B
9 <151> PRIOR FILING DATE: 2001-06-04
12 <160> NUMBER OF SEQ ID NOS: 23
13 <170> SOFTWARE: PatentIn version 3.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 114
17 <212> TYPE: PRT
18 <213> ORGANISM: Homo sapiens
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21 1 5 10 15
22 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
23 20 25 30
24 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
25 35 40 45
26 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
27 50 55 60
28 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
29 65 70 75 80
30 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
31 85 90 95
32 Val Lys Asp Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
33 100 105 110
34 Phe Asn
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41 <221> NAME/KEY: misc_feature
42 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Lys substitution at
43 residue 13
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45 Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu
46 1 5 10 15
47 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
48 20 25 30

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49      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
50              35              40              45
51      Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
52              50              55              60
53      Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
54      65              70              75              80
55      Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
56              85              90              95
57      Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
58              100              105              110
59      Phe Asn
61 <210> SEQ ID NO: 3
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63 <212> TYPE: PRT
64 <213> ORGANISM: ARTIFICIAL SEQUENCE
65 <220> FEATURE:
66 <221> NAME/KEY: misc_feature
67 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Ile substitution at
68     residue 13
69 <400> SEQUENCE: 3
70      Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ile Leu Ile Glu
71      1              5              10              15
72      Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
73              20              25              30
74      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
75              35              40              45
76      Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
77              50              55              60
78      Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
79      65              70              75              80
80      Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
81              85              90              95
82      Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
83              100              105              110
84      Phe Asn
86 <210> SEQ ID NO: 4
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88 <212> TYPE: PRT
89 <213> ORGANISM: ARTIFICIAL SEQUENCE
90 <220> FEATURE:
91 <221> NAME/KEY: misc_feature
92 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Cys substitution at
93     residue 13
94 <400> SEQUENCE: 4
95      Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Cys Leu Ile Glu
96      1              5              10              15
97      Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
98              20              25              30
99      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala

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100          35          40          45
101      Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
102          50          55          60
103      Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
104      65          70          75          80
105      Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
106          85          90          95
107      Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
108          100          105          110
109      Phe Asn
111 <210> SEQ ID NO: 5
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113 <212> TYPE: PRT
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115 <220> FEATURE:
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118      residue 13
119 <400> SEQUENCE: 5
120      Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ser Leu Ile Glu
121      1          5          10          15
122      Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
123          20          25          30
124      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
125          35          40          45
126      Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
127          50          55          60
128      Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
129      65          70          75          80
130      Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
131          85          90          95
132      Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
133          100          105          110
134      Phe Asn
136 <210> SEQ ID NO: 6
137 <211> LENGTH: 114
138 <212> TYPE: PRT
139 <213> ORGANISM: ARTIFICIAL SEQUENCE
140 <220> FEATURE:
141 <221> NAME/KEY: misc_feature
142 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Arg substitution at
143      residue 13
144 <400> SEQUENCE: 6
145      Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Arg Leu Ile Glu
146      1          5          10          15
147      Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
148          20          25          30
149      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
150          35          40          45

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151   Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
152       50                      55                      60
153   Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
154   65                      70                      75                      80
155   Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
156                      85                      90                      95
157   Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
158                      100                      105                      110
159   Phe Asn
161 <210> SEQ ID NO: 7
162 <211> LENGTH: 114
163 <212> TYPE: PRT
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165 <220> FEATURE:
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167 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Tyr substitution at
168   residue 13
169 <400> SEQUENCE: 7
170   Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Tyr Leu Ile Glu
171   1                      5                      10                      15
172   Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
173   20                      25                      30
174   Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
175   35                      40                      45
176   Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
177   50                      55                      60
178   Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
179   65                      70                      75                      80
180   Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
181   85                      90                      95
182   Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
183   100                      105                      110
184   Phe Asn
186 <210> SEQ ID NO: 8
187 <211> LENGTH: 114
188 <212> TYPE: PRT
189 <213> ORGANISM: ARTIFICIAL SEQUENCE
190 <220> FEATURE:
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192 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Asp substitution at
193   residue 13
194 <400> SEQUENCE: 8
195   Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Asp Leu Ile Glu
196   1                      5                      10                      15
197   Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
198   20                      25                      30
199   Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
200   35                      40                      45
201   Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr

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Input Set : N:\Crf3\RULE60\10053406.raw

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202          50          55          60
203      Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
204      65          70          75          80
205      Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
206          85          90          95
207      Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
208          100          105          110
209      Phe Asn
211 <210> SEQ ID NO: 9
212 <211> LENGTH: 114
213 <212> TYPE: PRT
214 <213> ORGANISM: ARTIFICIAL SEQUENCE
215 <220> FEATURE:
216 <221> NAME/KEY: misc_feature
217 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Lys substitution at
218      residue 16
219 <400> SEQUENCE: 9
220      Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Lys
221      1          5          10          15
222      Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
223          20          25          30
224      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
225          35          40          45
226      Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
227          50          55          60
228      Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
229      65          70          75          80
230      Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
231          85          90          95
232      Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
233          100          105          110
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239 <213> ORGANISM: ARTIFICIAL SEQUENCE
240 <220> FEATURE:
241 <221> NAME/KEY: misc_feature
242 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Lys substitution at
243      residue 17
244 <400> SEQUENCE: 10
245      Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
246      1          5          10          15
247      Lys Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
248          20          25          30
249      Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
250          35          40          45
251      Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
252          50          55          60

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VERIFICATION SUMMARY

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